



SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
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- (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS HAVING SERINE THREONINE KINASE DOMAINS, AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS:
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(F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/903,068
(B) FILING DATE: July 11, 2001
- (vii) PRIOR APPLICATION DATE:
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(A) APPLICATION NUMBER: PCT/GB93/02367
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- (x) PRIOR APPLICATION DATA:
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- (xi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304680.3
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 (A) APPLICATION NUMBER: 321344.5
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(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA	60
AGAAAACATTT TTGCTCCAGC CCCCATCCC A GTCCCCGGAG GCTGCCGCGC CAGCTGCC	120
GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGGCCGC GCCGGACCCC AGCCCGCCGT	180
CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA	240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC	294
	Met Thr Leu Gly
	1
TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG	342
Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln	
5 10 15 20	
GGA GAC CCT GTG AAG CCG TCT CCG GGC CCG CTG GTG ACC TGC ACG TGT	390
Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys	
25 30 35	
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA	438
Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr	
40 45 50	
GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC	486
Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly	
55 60 65	

TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC	534
Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe	
70 75 80	
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC	582
Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser	
85 90 95 100	
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT	630
Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp	
105 110 115	
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG	678
Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu	
120 125 130	
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG	726
Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu	
135 140 145	
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG	774
Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu	
150 155 160	
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT	822
Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser	
165 170 175 180	
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG	870
Asp Cys Thr Thr Gly Ser Gly Leu Pro Phe Leu Val Gln Arg	
185 190 195	
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC	918
Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	
200 205 210	
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC	966
Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val	
215 220 225	
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG	1014
Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu	
230 235 240	
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC	1062
Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile	
245 250 255 260	
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC	1110
Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile	
265 270 275	
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG	1158
Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln	
280 285 290	
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC	1206
Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys	
295 300 305	
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA	1254
Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro	
310 315 320	
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC	1302
Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser	
325 330 335 340	
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC GCT GTG ATG CAC TCA	1350
Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser	
345 350 355	
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC	1398
Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr	
360 365 370	

AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC	1446
Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp	
375 380 385	
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG	1494
Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val	
390 395 400	
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC	1542
Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp	
405 410 415 420	
TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG	1590
Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu	
425 430 435	
GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT	1638
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro	
440 445 450	
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG	1686
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met	
455 460 465	
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG	1734
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg	
470 475 480	
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA	1782
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys	
485 490 495 500	
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC	1831
Val Ile Gln	
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGTA GAGGTAGTGT GAGTGTGGTG	1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTGGCCCC CAGCCCACCC AGCCAAAAAT	1951
ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA	1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala	
1 5 10 15	
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val	
20 25 30	
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly	
35 40 45	
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln	
50 55 60	
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg	
65 70 75 80	
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn	
85 90 95	
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln	
100 105 110	
Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala	
115 120 125	
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg	
130 135 140	

Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
 145 150 155 160
 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
 165 170 175
 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
 180 185 190
 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
 195 200 205
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
 210 215 220
 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
 225 230 235 240
 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
 245 250 255
 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
 260 265 270
 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
 275 280 285
 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
 290 295 300
 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
 305 310 315 320
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
 325 330 335
 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
 340 345 350
 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
 355 360 365
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
 370 375 380
 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
 385 390 395 400
 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
 405 410 415
 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
 420 425 430
 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
 435 440 445
 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
 450 455 460
 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
 465 470 475 480
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
 485 490 495
 Glu Lys Pro Lys Val Ile Gln
 500

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104°.1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG
 GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA
 Met Val Asp Gly
 1
 GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT
 Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
 5 10 15 20
 ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG
 Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
 25 30 35
 TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG
 Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
 40 45 50
 TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA
 Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
 55 60 65
 GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG
 Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
 70 75 80
 CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC
 Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
 85 90 95 100
 AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA
 Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
 105 110 115
 ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG
 Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
 120 125 130
 TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA
 Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
 135 140 145
 TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT
 Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
 150 155 160
 GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA
 Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
 165 170 175 180
 GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT
 Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
 185 190 195
 CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG
 Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
 200 205 210
 TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA
 Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln
 215 220 225
 GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA
 Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser
 230 235 240
 TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA
 Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu
 250 255 260

245	250	255	260	
AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT				931
Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser				
265	270	275		
ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC				979
Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr				
280	285	290		
GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA				1027
Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile				
295	300	305		
GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT				1075
Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe				
310	315	320		
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA				1123
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys				
325	330	335	340	
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC				1171
Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly				
345	350	355		
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC				1219
Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn				
360	365	370		
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT				1267
Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp				
375	380	385		
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT				1315
Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile				
390	395	400		
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC				1363
Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser				
405	410	415	420	
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC				1411
Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro				
425	430	435		
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA				1459
Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln				
440	445	450		
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC				1507
Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr				
455	460	465		
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA				1555
Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala				
470	475	480		
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT				1603
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn				
485	490	495	500	
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA				1650
Ser Leu Asp Lys Leu Lys Thr Asp Cys				
505				
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT				1710
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC				1770
GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCAACCCTA ACCTCGCTCG ATGACTGTGA				1830
ACTGGGCATT TCACGAAC TGACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA				1890
AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG				1950
GCTTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT				2010
GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCTTTG				2070
CATTCCCTAAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTGCCAA AATGTTGGCT				2130

GCGTACTCCA	CTGGTCTGTC	TTGGATAAT	AGGAATTCAA	TTGGCAAAA	CAAAATGTAA	2190
TGTCAGACTT	TGCTGCATTT	TACACATGTG	CTGATGTTA	CAATGATGCC	GAACATTAGG	2250
AATTGTTAT	ACACAACCTT	GCAAATTATT	TATTACTTGT	GCACTTAGTA	GTTCACAA	2310
AACTGCTTG	TGCATATGTT	AAAGCTTATT	TTTATGTGGT	CTTATGATT	TATTACAGAA	2370
ATGTTTTAA	CACTATACTC	AAAATGGAC	ATTTCTTTT	ATTATCAGTT	AAAATCACAT	2430
TTAAGTGCT	TCACATTTGT	ATGTGTGTAG	ACTGTAACCTT	TTTTTCAGTT	CATATGCAGA	2490
ACGTATTTAG	CCATTACCCA	CGTGACACCA	CCGAATATAT	TATCGATTAA	GAAGCAAAGA	2550
TTTCAGTAGA	ATTTAGTCC	TGAACGCTAC	GGGGAAAATG	CATTTCTTC	AGAATTATCC	2610
ATTACGTGCA	TTTAAACTCT	GCCAGAAAAA	AATAACTATT	TTGTTTTAAT	CTACTTTTG	2670
TATTTAGTAG	TTATTTGTAT	AAATTAAATA	AACTGTTTC	AAGTCAAAAAA	AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu	
1				5					10				15			
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu	
				20				25				30				
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys	
	35				40				45							
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His	
	50				55					60						
Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr	
	65				70				75				80			
Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly	
			85					90				95				
Asp	Trp	Cys	Asn	Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys	
		100				105					110					
Ser	Phe	Pro	Gly	Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile	
		115				120					125					
Leu	Ser	Val	Val	Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val	
		130				135					140					
Ala	Leu	Arg	Lys	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg	
	145				150				155				160			
Asp	Val	Glu	Tyr	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly	
		165				170					175					
Asp	Ser	Thr	Leu	Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser	
		180				185					190					
Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile	
		195				200				205						
Thr	Leu	Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	
	210				215				220							
Gly	Ser	Trp	Gln	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	
	225				230				235				240			
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met	
		245				250					255					
Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	
		260				265					270					
Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met	
		275				280					285					
Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser	
		290				295				300						

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
 305 310 315 320
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
 325 330 335
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
 340 345 350
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
 355 360 365
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
 370 375 380
 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
 385 390 395 400
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
 405 410 415
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
 420 425 430
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
 435 440 445
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
 450 455 460
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
 465 470 475 480
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
 485 490 495
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
 500 505

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2932 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 310..1905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT	60
CAGTTTAATA CTGTCTTGGAA ATTCACTGAGA TGGAAAGCATA GGTCAAAGCT GTTGGAGAA	120
AATCAGAACT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG	180
TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA	240
TTTAAATTGG TGAAGTAGCA AGACCAATTAA TTAAAGGTGA CAGTACACAG GAAACATTAC	300
AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC	348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala	
1 5 10	
TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG	396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met	
15 20 25	
CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA	444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Ser Glu	

30	35	40	45	
AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC				492
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys				
50	55	60		
TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA				540
Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile				
65	70	75		
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA				588
Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu				
80	85	90		
ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG				636
Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln				
95	100	105		
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT				684
Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys				
110	115	120	125	
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT				732
Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val				
130	135	140		
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC				780
Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu				
145	150	155		
ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC				828
Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys				
160	165	170		
TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC				876
Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Arg Tyr				
175	180	185		
AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA				924
Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser				
190	195	200	205	
CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA				972
Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly				
210	215	220		
CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC				1020
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val				
225	230	235		
CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG				1068
Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp				
240	245	250		
CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC				1116
Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala				
255	260	265		
AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT				1164
Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His				
270	275	280	285	
GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC				1212
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser				
290	295	300		
TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC				1260
Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu				
305	310	315		
TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA				1308
Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys				
320	325	330		
TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT				1356
Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile				

335	340	345	
TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC			1404
Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser			
350	355	360	365
AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG			1452
Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu			
370	375	380	
GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC			1500
Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro			
385	390	395	
TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG			1548
Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu			
400	405	410	
GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC			1596
Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp			
415	420	425	
ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC			1644
Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile			
430	435	440	445
ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA			1692
Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val			
450	455	460	
CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA			1740
Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys			
465	470	475	
CGT TTG CCG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA			1788
Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu			
480	485	490	
CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC			1836
Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala			
495	500	505	
TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT			1884
Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val			
510	515	520	525
GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT			1935
Glu Ser Gln Asp Val Lys Ile			
530			
AGACTGCAAG AACTGTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT			1995
AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTCACAG GCTGCTAATA TTAAACCTTT			2055
CAGTACTCTT ATTAGGATAC AAGCTGGAA CTTCTAAACA CTTCATTCTT TATATATGGAA			2115
CAGCTTTATT TTAAATGTGG TTTTGATGC CTTTTTTAA GTGGGTTTT ATGAAGTGC			2175
TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTT			2235
ATAAAACGGT GCTTCTGT AAAGCCTAA GAAGATAAT GAGCGCAGCA GAGATGGAGA			2295
AATAGACTTT GCCTTTTACC TGAGACATTG AGTCGTTTG TATTCTACCT TTGAAAACA			2355
GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTAA TGATAGTTG TCCTGTGTCC			2415
TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCCTCTGC TGCCATTG			2475
ATTAGAAGAA AATAATTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTG			2535
CTTTAAAAAT GCAATATCTG ACCAAGATTG GCCAATCTCA TACAAGCCAT TTACTTGCA			2595
AGTGAGATAG CTTCCCCACC AGCTTTATT TTTAACATGA AAGCTGATGC CAAGGCCAA			2655
AGAAGTTAA AGCATCTGTA AATTGGACT GTTTCCCTTC AACCAACATT TTTTTGTGG			2715
TTATTATTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC			2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCCT GCATTTGATA GCAATGTAAG			2835
TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAAC TTTAAAAGGG AAGTTATTAA			2895
TATTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC			2932

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe
1 5 10 15
Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
20 25 30
Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val
35 40 45
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
50 55 60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
65 70 75 80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
85 90 95
Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
100 105 110
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
115 120 125
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
130 135 140
Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile Ser Met
145 150 155 160
Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
165 170 175
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn Arg Asp
180 185 190
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
195 200 205
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Leu Pro Leu
210 215 220
Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
225 230 235 240
Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
245 250 255
Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
260 265 270
Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
275 280 285
Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
290 295 300
Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
305 310 315 320
Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
325 330 335
Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
340 345 350
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
355 360 365
Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
370 375 380
Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr
385 390 395 400
Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser

405	410	415
Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser		
420	425	430
Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly		
435	440	445
Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp		
450	455	460
Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg		
465	470	475
Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val		
485	490	495
Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu		
500	505	510
Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln		
515	520	525
Asp Val Lys Ile		
530		

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC	48		
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu			
1	5	10	15
CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG GTC CAG GCT CTG	96		
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Val Gln Ala Leu			
20	25	30	
CTG TGT GCG TGC ACC AGC TGC CTC CAG GCC AAC TAC ACG TGT GAG ACA	144		
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr			
35	40	45	
GAT GGG GCC TGC ATG GTT TCC TTT TTC AAT CTG GAT GGG ATG GAG CAC	192		
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His			
50	55	60	
CAT GTG CGC ACC TGC ATC CCC AAA GTG GAG CTG GTC CCT GCC GGG AAG	240		
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys			
65	70	75	80
CCC TTC TAC TGC CTG AGC TCG GAG GAC CTG CGC AAC ACC CAC TGC TGC	288		
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys			
85	90	95	
TAC ACT GAC TAC TGC AAC AGG ATC GAC TTG AGG GTG CCC AGT GGT CAC	336		
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His			
100	105	110	
CTC AAG GAG CCT GAG CAC CCG TCC ATG TGG GGC CCG GTG GAG CTG GTA	384		

Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
115								120					125		
GGC	ATC	ATC	GCC	GGC	CCG	GTG	TTC	CTC	CTG	TTC	CTC	ATC	ATC	ATC	ATT
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile
130							135					140			
GTT	TTC	CTT	GTC	ATT	AAC	TAT	CAT	CAG	CGT	GTC	TAT	CAC	AAC	CGC	CAG
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln
145							150				155			160	
AGA	CTG	GAC	ATG	GAA	GAT	CCC	TCA	TGT	GAG	ATG	TGT	CTC	TCC	AAA	GAC
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp
						165				170			175		
AAG	ACG	CTC	CAG	GAT	CTT	GTC	TAC	GAT	CTC	TCC	ACC	TCA	GGG	TCT	GGC
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly
						180				185			190		
TCA	GGG	TTA	CCC	CTC	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	ACC	ATC	GTT
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val
						195				200			205		
TTA	CAA	GAG	ATT	ATT	GGC	AAG	GGT	CGG	TTT	GGG	GAA	GTA	TGG	CGG	GGC
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly
						210				215			220		
CGC	TGG	AGG	GGT	GGT	GAT	GTG	GCT	GTG	AAA	ATA	TTC	TCT	TCT	CGT	GAA
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu
						225				230			235		240
GAA	CGG	TCT	TGG	TTC	AGG	GAA	GCA	GAG	ATA	TAC	CAG	ACG	GTC	ATG	CTG
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu
						245				250			255		
CGC	CAT	GAA	AAC	ATC	CTT	GGA	TTT	ATT	GCT	GCT	GAC	AAT	AAA	GAT	AAT
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn
						260				265			270		
GGC	ACC	TGG	ACA	CAG	CTG	TGG	CTT	GTT	TCT	GAC	TAT	CAT	GAG	CAC	GGG
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly
						275				280			285		
TCC	CTG	TTT	GAT	TAT	CTG	AAC	CGG	TAC	ACA	GTG	ACA	ATT	GAG	GGG	ATG
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met
						290				295			300		
ATT	AAG	CTG	GCC	TTG	TCT	GCT	GCT	AGT	GGG	CTG	GCA	CAC	CTG	CAC	ATG
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met
						305				310			315		320
GAG	ATC	GTG	GGC	ACC	CAA	GGG	AAG	CCT	GGA	ATT	GCT	CAT	CGA	GAC	TTA
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu
						325				330			335		
AAG	TCA	AAG	AAC	ATT	CTG	GTG	AAG	AAA	AAT	GGC	ATG	TGT	GCC	ATA	GCA
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala
						340				345			350		
GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCA	GTC	ACT	GAC	ACC	ATT	GAC
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp
						355				360			365		
ATT	GCC	CCG	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	GCC	CCT	GAA
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu
						370				375			380		
GTA	CTT	GAT	GAA	ACC	ATT	AAT	ATG	AAA	CAC	TTT	GAC	TCC	TTT	AAA	TGT
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys
						385				390			395		400
GCT	GAT	ATT	TAT	GCC	CTC	GGG	CTT	GTA	TAT	TGG	GAG	ATT	GCT	CGA	AGA
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg
						405				410			415		
TGC	AAT	TCT	GGA	GGG	GTC	CAT	GAA	GAA	TAT	CAG	CTG	CCA	TAT	TAC	GAC

Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp		
420	425	430
TTA GTG CCC TCT GAC CCT TCC ATT GAG GAA ATG CGA AAG GTT GTA TGT		1344
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys		
435	440	445
GAT CAG AAG CTG CGT CCC AAC ATC CCC AAC TGG TGG CAG AGT TAT GAG		1392
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu		
450	455	460
GCA CTG CGG GTG ATG GGG AAG ATG ATG CGA GAG TGT TGG TAT GCC AAC		1440
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn		
465	470	475
GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAC ACC CTC TCC CAG		1488
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln		
485	490	495
CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC		1535
Leu Ser Val Gln Glu Asp Val Lys Ile		
500	505	
ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC GATGGAGGCC		1595
TACCTCTCGT TTCTGCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA GAGGGACAGA		1655
GCCCCGGAGA GACTCGCTCA CTCCCATGTT GGGTTTGAGA CAGACACCTT TTCTATTTAC		1715
CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG CCACACCTCG		1775
AACTGGTTGT AGTGGGAAGT CCCGCGAAAC CCGGTGCATC TGCCACGTGG CCAGGAGCCA		1835
TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT AAGCTGCCCT		1895
GAGGGTTTCC TTCGGGGACC AGCCCCACAGC ACACCAAGGT GGCCCGGAAG AACCAAAGT		1955
GCAGCCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTTCCCC TCCTCCCTGG GATGGACGCT		2015
GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTGT CTGTCAGGCC GTGTGTGCAT		2075
GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCTGTGCCAT GCCCTTACAC GTGCGTGTGA		2135
GTGTGTGTGT GTGTCTGTAG GTGCGCACCT ACCTGCTTGA GCTTTCTGTG CATGTGCAGG		2195
TCGGGGGTGT GGTCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTTCAG TAGTGAGCAG		2255
CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCCAGAG CCCCTCATGC		2315
CACAGTGGTA CTCTGTGT		2333

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu		
1	5	10
15		
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Val Gln Ala Leu		
20	25	30
25		
Leu Cys Ala Cys Thr Ser Cys Leu Gln Ala Asn Tyr Thr Cys Glu Thr		
35	40	45
40		
Asp Gly Ala Cys Met Val Ser Phe Phe Asn Leu Asp Gly Met Glu His		
50	55	60
55		
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys		
65	70	75
70		
80		
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys		
85	90	95
90		
Tyr Thr Asp Tyr Cys Asn Arg Ile Asp Leu Arg Val Pro Ser Gly His		
100	105	110
105		
Leu Lys Glu Pro Glu His Pro Ser Met Trp Gly Pro Val Glu Leu Val		
115	120	125
120		
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile		

130	135	140
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val	Tyr His Asn Arg Gln	
145	150	155
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu	Met Cys Leu Ser Lys Asp	160
165	170	175
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser	Thr Ser Gly Ser Gly	
180	185	190
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val	Ala Arg Thr Ile Val	
195	200	205
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe	Gly Glu Val Trp Arg Gly	
210	215	220
Arg Trp Arg Gly Gly Asp Val Ala Val Lys	Ile Phe Ser Ser Arg Glu	
225	230	235
Glu Arg Ser Trp Phe Arg Glu Ala Glu	Ile Tyr Gln Thr Val Met Leu	240
245	250	255
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala	Asp Asn Lys Asp Asn	
260	265	270
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp	Tyr His Glu His Gly	
275	280	285
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val	Thr Ile Glu Gly Met	
290	295	300
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly	Leu Ala His Leu His Met	
305	310	315
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly	Ile Ala His Arg Asp Leu	320
325	330	335
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly	Met Cys Ala Ile Ala	
340	345	350
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val	Thr Asp Thr Ile Asp	
355	360	365
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg	Tyr Met Ala Pro Glu	
370	375	380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe	Asp Ser Phe Lys Cys	
385	390	395
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp	Glu Ile Ala Arg Arg	
405	410	415
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln	Leu Pro Tyr Tyr Asp	
420	425	430
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met	Arg Lys Val Val Cys	
435	440	445
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp	Trp Gln Ser Tyr Glu	
450	455	460
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu	Cys Trp Tyr Ala Asn	
465	470	475
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys	Lys Thr Leu Ser Gln	480
485	490	495
Leu Ser Val Gln Glu Asp Val Lys Ile		
500	505	

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCGAGGCAG	GGTTTGCTGG	GGTGAGGCAG	CGGCGCGGCC	GGGCCGGGCC	GGGCCACAGG	60
CGGTGGCGGC	GGGACC	ATG GAG	GCG GCG	GTC GCT	CCG CGT CCC CGG	109
Met Glu Ala Ala Val	Ala Ala Ala Pro	Arg Pro Arg				
1	5	10				
CTG CTC CTC CTC	GTG CTG GCG	GCG GCG GCG	GCG GCG GCG	GCG GCG GCG	CTG	157
Leu Leu Leu Leu	Val Leu Ala Ala	Ala Ala Ala Ala	Ala Ala Ala Ala	Ala Ala Ala	Leu	
15	20	25				
CTC CCG GGG GCG	ACG GCG TTA	CAG TGT TTC	TGC CAC CTC	TGT ACA AAA		205
Leu Pro Gly Ala	Thr Ala Leu	Gln Cys Phe	Cys His Leu	Cys Thr Lys		
30	35	40				
GAC AAT TTT ACT	TGT GTG ACA GAT	GGG CTC TGC	TTT GTC TCT	GTC ACA		253
Asp Asn Phe Thr	Cys Val Thr Asp	Gly Leu Cys	Phe Val Ser	Val Thr		
45	50	55				
GAG ACC ACA GAC	AAA GTT ATA CAC AAC	AGC ATG TGT	ATA GCT GAA ATT			301
Glu Thr Thr Asp	Lys Val Ile His	Asn Ser Met	Cys Ile Ala	Glu Ile		
60	65	70	75			
GAC TTA ATT CCT CGA	GAT AGG CCG TTT	GTA TGT GCA	CCC TCT TCA	AAA		349
Asp Leu Ile Pro	Arg Asp Arg Pro	Phe Val Cys	Ala Pro Ser	Ser Lys		
80	85	90				
ACT GGG TCT GTG	ACT ACA ACA TAT	TGC TGC AAT	CAG GAC CAT	TGC AAT		397
Thr Gly Ser Val	Thr Thr Tyr Cys	Cys Asn Gln	Asp His Cys	Asn		
95	100	105				
AAA ATA GAA CTT CCA	ACT ACT GTA AAG	TCA TCA CCT GGC	CTT GGT CCT			445
Lys Ile Glu Leu	Pro Thr Thr Val	Lys Ser Ser	Pro Gly Leu	Gly Pro		
110	115	120				
GTG GAA CTG GCA	GCT GTC ATT GCT	GGA CCA GTG	TGC TTC GTC	TGC ATC		493
Val Glu Leu Ala	Ala Val Ile Ala	Gly Pro Val	Cys Phe Val	Cys Ile		
125	130	135				
TCA CTC ATG TTG ATG	GTC TAT ATC TGC	CAC AAC CGC	ACT GTC ATT CAC			541
Ser Leu Met Leu	Met Val Tyr Ile	Cys His Asn	Arg Thr Val	Ile His		
140	145	150	155			
CAT CGA GTG CCA	AAT GAA GAG GAC	CCT TCA TTA	GAT CGC CCT	TTT ATT		589
His Arg Val Pro	Asn Glu Glu Asp	Pro Ser Leu	Asp Arg Pro	Phe Ile		
160	165	170				
TCA GAG GGT ACT	ACG TTG AAA GAC	TTA ATT TAT	GAT ATG ACA ACG	TCA		637
Ser Glu Gly Thr	Thr Leu Lys Asp	Leu Ile Tyr	Asp Met	Thr Thr Ser		
175	180	185				
GGT TCT GGC TCA	GGT TTA CCA TTG	CTT GTT CAG AGA	ACA ATT GCG AGA			685
Gly Ser Gly Ser	Gly Leu Pro Leu	Leu Val Gln	Arg Thr Ile	Ala Arg		
190	195	200				
ACT ATT GTG TTA	CAA GAA AGC ATT	GGC AAA GGT	CGA TTT GGA GAA	GTT		733
Thr Ile Val Leu	Gln Glu Ser Ile	Gly Lys Gly	Arg Phe	Gly Glu Val		
205	210	215				
TGG AGA GGA AAG	TGG CGG GGA GAA	GAA GTT GCT	GTT AAG ATA TTC	TCC		781
Trp Arg Gly Lys	Trp Arg Gly	Glu Glu Val	Ala Val Lys	Ile Phe Ser		
220	225	230	235			
TCT AGA GAA GAA	CGT TCG TGG TTC	CGT GAG GCA	GAG ATT TAT	CAA ACT		829
Ser Arg Glu Glu	Arg Ser Trp Phe	Arg Glu Ala	Glu Ile Tyr	Gln Thr		
240	245	250				
GTA ATG TTA CGT	CAT GAA AAC ATC	CTG GGA	TTT ATA GCA	GCA GAC AAT		877

Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	
255								260						265		
AAA	GAC	AAT	GGT	ACT	TGG	ACT	CAG	CTC	TGG	TTG	GTG	TCA	GAT	TAT	CAT	925
Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	
270							275				280					
GAG	CAT	GGA	TCC	CTT	TTT	GAT	TAC	TTA	AAC	AGA	TAC	ACA	GTT	ACT	GTG	973
Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	
285							290				295					
GAA	GGA	ATG	ATA	AAA	CTT	GCT	CTG	TCC	ACG	GCG	AGC	GGT	CTT	GCC	CAT	1021
Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	
300							305				310				315	
CTT	CAC	ATG	GAG	ATT	GTT	GGT	ACC	CAA	GGA	AAG	CCA	GCC	ATT	GCT	CAT	1069
Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	
320							325							330		
AGA	GAT	TTG	AAA	TCA	AAG	AAT	ATC	TTG	GTA	AAG	AAG	AAT	GGA	ACT	TGC	1117
Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	
335							340							345		
TGT	ATT	GCA	GAC	TTA	GGA	CTG	GCA	GTA	AGA	CAT	GAT	TCA	GCC	ACA	GAT	1165
Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	
350							355							360		
ACC	ATT	GAT	ATT	GCT	CCA	AAC	CAC	AGA	GTG	GGA	ACA	AAA	AGG	TAC	ATG	1213
Thr	Ile	Asp	Ile	Ala	Pro	Asn	His	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	
365							370							375		
GCC	CCT	GAA	GTT	CTC	GAT	GAT	TCC	ATA	AAT	ATG	AAA	CAT	TTT	GAA	TCC	1261
Ala	Pro	Glu	Val	Leu	Asp	Asp	Ser	Ile	Asn	Met	Lys	His	Phe	Glu	Ser	
380							385				390				395	
TTC	AAA	CGT	GCT	GAC	ATC	TAT	GCA	ATG	GGC	TTA	GTA	TTC	TGG	GAA	ATT	1309
Phe	Lys	Arg	Ala	Asp	Ile	Tyr	Ala	Met	Gly	Leu	Val	Phe	Trp	Glu	Ile	
400							405							410		
GCT	CGA	CGA	TGT	TCC	ATT	GGT	GGA	ATT	CAT	GAA	GAT	TAC	CAA	CTG	CCT	1357
Ala	Arg	Arg	Cys	Ser	Ile	Gly	Gly	Ile	His	Glu	Asp	Tyr	Gln	Leu	Pro	
415							420							425		
TAT	TAT	GAT	CTT	GTA	CCT	TCT	GAC	CCA	TCA	GTT	GAA	GAA	ATG	AGA	AAA	1405
Tyr	Tyr	Asp	Leu	Val	Pro	Ser	Asp	Pro	Ser	Val	Glu	Glu	Met	Arg	Lys	
430							435							440		
GTT	GTT	TGT	GAA	CAG	AAG	TTA	AGG	CCA	AAT	ATC	CCA	AAC	AGA	TGG	CAG	1453
Val	Val	Cys	Glu	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Gln	
445							450							455		
AGC	TGT	GAA	GCC	TTG	AGA	GTA	ATG	GCT	AAA	ATT	ATG	AGA	GAA	TGT	TGG	1501
Ser	Cys	Glu	Ala	Leu	Arg	Val	Met	Ala	Lys	Ile	Met	Arg	Glu	Cys	Trp	
460							465				470				475	
TAT	GCC	AAT	GGA	GCA	GCT	AGG	CTT	ACA	GCA	TTG	CGG	ATT	AAG	AAA	ACA	1549
Tyr	Ala	Asn	Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	
480							485							490		
TTA	TCG	CAA	CTC	AGT	CAA	CAG	GAA	GGC	ATC	AAA	ATG	TAATTCTACA				1595
Leu	Ser	Gln	Leu	Ser	Gln	Gln	Glu	Ile	Lys	Met						
495							500									
GCTTGCCTG	AACTCTCCTT	TTTTCTTCAG	ATCTGCTCCT	GGGTTTTAAT	TTGGGAGGTC											1655
AGTTGTTCTA	CCTCACTGAG	AGGGAACAGA	AGGATATTGC	TTCTTTTTCG	AGCAGTGTAA											1715
TAAAGTCAAT	AAAAAACTTC	CCAGGATTTTC	TTTGACCCA	GGAAACAGCC	ATGTGGGTCC											1775
TTTCTGTGCA	CTATGAACGC	TTCTTTCCA	GGACAGAAAA	TGTGTAGTCT	ACCTTTATT											1835
TTTATTAACA	AAACTTGT	TTTAAAAAGA	TGATTGCTGG	TCTTAAC	TTT	AGGTAAC	CT	TT	AGT	CT	TT	AGT	CT	TT	AGT	1895
GCTGTGCTGG	AGATCATCTT	TAAGGGCAA	GGAGTTGGAT	TGCTGA	ATTA	CAATGAA	ACA	CA	ATG	AA	CTG	AA	CTG	AA	CTG	1955
TGTCTTATT	CTAAAGAAAG	TGATTTACTC	CTGGTAGTA	CATTCTCAGA	GGATT	CTGAA	CA	ATG	AA	CTG	AA	CTG	AA	CTG	AA	2015
CCACTAGAGT	TTCCTTGATT	CAGACTTTGA	ATGTACTGTT	CTATAGTT	TTT	TCAGGAT	CTT	AGT	TTT	TCAGGAT	CTT	AGT	TTT	TCAGGAT	CTT	2075
AAAACATAACA	CTTATAAACAC	TCTTATCTTG	AGTCTAAAAA	TGACCTCATA	TAGTAGT	GAG	CT	AC	TA	TGACCTCATA	TAGTAGT	GAG	CT	AC	TA	2135
GAACATAATT	CATGCAATTG	TATTTGTAT	ACTATTATTG	TTCTTCACT	TATT	CAGAAC	AC	TA	TT	CTCAGAAC	AC	TA	TT	CTCAGAAC	AC	2195

ATTACATGCC TTCAAAATGG GATTGTACTA TACCAAGTAAG TGCCACTTCT GTGTCTTTCT
AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT

2255
2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg Leu Leu Leu Leu Val
1 5 10 15
Leu Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly Ala Thr
20 25 30
Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn Phe Thr Cys
35 40 45
Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys
50 55 60
Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg
65 70 75 80
Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr
85 90 95
Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro
100 105 110
Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala
115 120 125
Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met
130 135 140
Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn
145 150 155 160
Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr
165 170 175
Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly
180 185 190
Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln
195 200 205
Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp
210 215 220
Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg
225 230 235 240
Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His
245 250 255
Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr
260 265 270
Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu
275 280 285
Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys
290 295 300
Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile
305 310 315 320
Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser
325 330 335
Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu
340 345 350
Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala
355 360 365

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu
 370 375 380
 Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp
 385 390 395 400
 Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser
 405 410 415
 Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val
 420 425 430
 Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln
 435 440 445
 Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu
 450 455 460
 Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
 465 470 475 480
 Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
 485 490 495
 Gln Gln Glu Gly Ile Lys Met
 500

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1922 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG	CCCTTCCAG	TCCCCGGAGC	CGCCGCGCCA	CGCGCGCATG	ATCAAGACCT	60
TTTCCCCGGC	CCCACAGGGC	CTCTGGACGT	GAGACCCCGG	CCGCCTCCGC	AAGGAGAGGC	120
GGGGGTGAG	TCGCCCTGTC	CAAAGGCCTC	AATCTAAACA	ATCTTGATTC	CTGTTGCCGG	180
CTGGCGGGAC	CCTGAATGGC	AGGAAATCTC	ACCACATCTC	TTCTCCTATC	TCCAAGGACC	240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC						288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala						
1 .	5	10	15			
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC						336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn						
20	25	30				
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA						384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser						
35	40	45				
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC						432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val						
50	55	60				
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC						480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro						
65	70	75	80			
ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC						528
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His						

	85	90	95	
AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA				576
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro				
100	105	110		
GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG				624
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu				
115	120	125		
CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG				672
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg				
130	135	140		
AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT				720
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser				
145	150	155	160	
CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC				768
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe				
165	170	175		
CTG GAC AGC GAC TGT ACC ACG GGC AGC GGC TCG GGG CTC CCC TTC TTG				816
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu				
180	185	190		
GTG CAG AGG ACG GTA GCT CGG CAG GTT GCG CTG GTA GAG TGT GTG GGA				864
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly				
195	200	205		
AAG GGC CGA TAT GGC GAG GTG TGG CGC GGT TCG TGG CAT GGC GAA AGC				912
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser				
210	215	220		
GTG GCG GTC AAG ATT TTC TCC TCA CGA GAT GAG CAG TCC TGG TTC CGG				960
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg				
225	230	235	240	
GAG ACG GAG ATC TAC AAC ACA GTT CTG CTT AGA CAC GAC AAC ATC CTA				1008
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu				
245	250	255		
GGC TTC ATC GCC TCC GAC ATG ACT TCG CGG AAC TCG AGC ACG CAG CTG				1056
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu				
260	265	270		
TGG CTC ATC ACC CAC TAC CAT GAA CAC GGC TCC CTC TAT GAC TTT CTG				1104
Trp Leu Ile Thr His Tyr His Glu His Ser Leu Tyr Asp Phe Leu				
275	280	285		
CAG AGG CAG ACG CTG GAG CCC CAG TTG GCC CTG AGG CTA GCT GTG TCC				1152
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser				
290	295	300		
CCG GCC TGC GGC CTG GCG CAC CTA CAT GTG GAG ATC TTT GGC ACT CAA				1200
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln				
305	310	315	320	
GGC AAA CCA GCC ATT GCC CAT CGT GAC CTC AAG AGT CGC AAT GTG CTG				1248
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu				
325	330	335		
GTC AAG AGT AAC TTG CAG TGT TGC ATT GCA GAC CTG GGA CTG GCT GTG				1296
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val				
340	345	350		
ATG CAC TCA CAA AGC AAC GAG TAC CTG GAT ATC GGC AAC ACA CCC CGA				1344
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg				
355	360	365		
GTG GGT ACC AAA AGA TAC ATG GCA CCC GAG GTG CTG GAT GAG CAC ATC				1392
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile				
370	375	380		
CGC ACA GAC TGC TTT GAG TCG TAC AAG TGG ACA GAC ATC TGG GCC TTT				1440
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe				

385	390	395	400	
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT		Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile		1488
	405		410	415
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC		Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro		1536
	420		425	430
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC		Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro		1584
	435		440	445
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC		Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala		1632
	450		455	460
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC		Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr		1680
	465		470	475
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG		Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu		1728
	485		490	495
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCCAGGCT TCCTCTGCCT		Lys Pro Lys Val Ile His		1776
	500			
AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGTA GAGGGAGTGA AGAGAGTGTG		CACGCTGCCCT TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC		1836
		TGAGCTGAAA TTCAAAAAAA AAAAAAA		1896
				1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid .
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Thr	Leu	Gly	Ser	Phe	Arg	Arg	Gly	Leu	Leu	Met	Leu	Ser	Val	Ala	
1																15
Leu	Gly	Leu	Thr	Gln	Gly	Arg	Leu	Ala	Lys	Pro	Ser	Lys	Leu	Val	Asn	
20																30
Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Arg	Pro	Phe	Cys	Gln	Gly	Ser	
35																45
Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Gln	Gly	Arg	His	Pro	Gln	Val	
50																60
Tyr	Arg	Gly	Cys	Gly	Ser	Leu	Asn	Gln	Glu	Leu	Cys	Leu	Gly	Arg	Pro	
65																80
Thr	Glu	Phe	Leu	Asn	His	His	Cys	Cys	Tyr	Arg	Ser	Phe	Cys	Asn	His	
85																95
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro	
100																110
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	
115																125
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg	
130																140
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser	
145																160
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe	
165																175
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	

180	185	190
Val Gln Arg Thr Val Ala Arg Gln	Val Ala Leu Val Glu Cys Val Gly	
195	200	205
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser		
210	215	220
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg		
225	230	235
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu		
245	250	255
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu		
260	265	270
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu		
275	280	285
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser		
290	295	300
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln		
305	310	315
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu		
325	330	335
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val		
340	345	350
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg		
355	360	365
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile		
370	375	380
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe		
385	390	395
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile		
405	410	415
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro		
420	425	430
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro		
435	440	445
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala		
450	455	460
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr		
465	470	475
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu		
485	490	495
Lys Pro Lys Val Ile His		
500		

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2070 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTCATGAGA TCCAAGCATA GGTCAAAGCT GTTGGAGAA ATTGGAACTA CAGTTTATC	60
TAGCCACATC TCTGAGAATT CTGAAGAAAG CAGCAGGTGA AAGTCATTGC CAAGTGATTT	120
TGTTCTGTAA GGAAGCCTCC CTCATTCACT TACACCAGTG AGACAGCAGG ACCAGTCATT	180
CAAAGGGCCG TGTACAGGAC GCGTGGCAAT CAGACA ATG ACT CAG CTA TAC ACT	234
Met Thr Gln Leu Tyr Thr	
1 5	
TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA	282
Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln	
10 15 20	
GGG CAG AAT CTA GAT AGT ATG CTC CAT GGC ACT GGT ATG AAA TCA GAC	330
Gly Gln Asn Leu Asp Ser Met Leu His Gly Thr Gly Met Lys Ser Asp	
25 30 35	
TTG GAC CAG AAG CCA GAA AAT GGA GTG ACT TTA GCA CCA GAG GAT	378
Leu Asp Gln Lys Lys Pro Glu Asn Gly Val Thr Leu Ala Pro Glu Asp	
40 45 50	
ACC TTG CCT TTC TTA AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT	426
Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp	
55 60 65 70	
GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA	474
Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile	
75 80 85	
GAA GAA GAT GAT CAG GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG	522
Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys	
90 95 100	
TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA	570
Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu	
105 110 115	
CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG	618
Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu	
120 125 130	
CAG CCT ACA CTG CCC CCT GTT ATA GGT CCG TTC TTT GAT GGC AGC	666
Gln Pro Thr Leu Pro Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser	
135 140 145 150	
ATC CGA TGG CTG GTT CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT	714
Ile Arg Trp Leu Val Leu Ile Ser Met Ala Val Cys Ile Val Ala	
155 160 165	
ATG ATC ATC TTC TCC AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT	762
Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser	
170 175 180	
ATC TCA AGC AGG GGT CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA	810
Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala	
185 190 195	
TTT ATT CCA GTA GGA GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA	858
Phe Ile Pro Val Gly Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln	
200 205 210	
AGC TCT GGG AGT GGA TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT	906
Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile	
215 220 225 230	
GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA	954
Ala Lys Gln Ile Gln Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly	
235 240 245	
GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG	1002
Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val	
250 255 260	
TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC	1050

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Thr Gln Leu Tyr Thr Ile Arg Leu Leu Gly Ala Cys Leu Phe
1 5 10 15
Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
20 25 30
Thr Gly Met Lys Ser Asp Leu Asp Gln Lys Lys Pro Glu Asn Gly Val
35 40 45
Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
50 55 60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
65 70 75 80
His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
85 90 95
Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
100 105 110
Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
115 120 125
Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
130 135 140
Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Val Leu Ile Ser Met
145 150 155 160
Ala Val Cys Ile Val Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
165 170 175
Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp
180 185 190
Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
195 200 205
Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
210 215 220
Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
225 230 235 240
Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
245 250 255
Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
260 265 270
Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
275 280 285
Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
290 295 300
Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
305 310 315 320
Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
325 330 335
Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
340 345 350
Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
355 360 365
Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
370 375 380
Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr
385 390 395 400

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
 485 490 495
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
 500 505 510
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
 515 520 525
 Asp Val Lys Ile
 530

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC CCC CTT	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu	
1 5 10	
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC	96
Val Val Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile	
15 20 25	
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC	144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr	
30 35 40 45	
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	

AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG	384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val	
110 115 120 125	
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC	432
Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile	
130 135 140	
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT	480
Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His	
145 150 155	
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC	528
Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu	
160 165 170	
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA	576
Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser	
175 180 185	
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA	624
Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg	
190 195 200 205	
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA	672
Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val	
210 215 220	
TGG CGT GGT CGC TGG AGG GGT GAC GTG GCT GTG AAA ATC TTC TCT	720
Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser	
225 230 235	
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC	768
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr	
240 245 250	
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT	816
Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
255 260 265	
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC	864
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
270 275 280 285	
GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT	912
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile	
290 295 300	
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC	960
Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His	
305 310 315	
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT	1008
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His	
320 325 330	
CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT	1056
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys	
335 340 345	
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC	1104
Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp	
350 355 360 365	
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG	1152
Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met	
370 375 380	
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC	1200
Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser	
385 390 395	
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT	1248
Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile	
400 405 410	

GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG	1296
Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG	1344
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys	
430 435 440 445	
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG	1392
Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln	
450 455 460	
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG	1440
Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp	
465 470 475	
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT	1488
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC	1534
Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile	
495 500 505	
CTCTGCCTAC ACAAAAGAACCGGGCAGTGA GGATGACTGC AGGCCACCGTG CAAGCGTCGT	1594
GGAGGCCTAT CCTCTTGTCTT CTGCCCCGGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGG	1654
CAGAGCCTGG GAGACCGCGC CACTCCCCTT GGGTTTGAGA CAGACACTTT TTATATTTAC	1714
CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACCTCAAAC	1774
GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG	1834
CTCGCCAGGA GCGGCCCGCCA TACCTTGTGG TCCACTGGGC TGCAAGGTTTT CCTCCAGGG	1894
CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC TTCCCGTAGC	1954
AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCTA GAGACACAAC	2014
CTGCTGCCTG TCTGTCCAGC CAAGTGCAGCA TGTGCCGAGG TGTGTCCCCAC ATTGTGCCTG	2074
GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACACTTA	2134
ACCTGCTTGA GCTTCTGTGC ATGTGT	2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu	
1 5 10 15	
Leu Leu Ala Gly Ser Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu	
20 25 30	
Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr	
35 40 45	
Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His	
50 55 60	
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys	
65 70 75 80	
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys	
85 90 95	
Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His	
100 105 110	
Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val	
115 120 125	
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile	
130 135 140	
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln	

145	150	155	160
Arg Leu Asp Met Glu Asp Pro Ser Cys	Glu Met Cys Leu Ser Lys Asp		
165	170	175	
Lys Thr Leu Gln Asp Leu Val Tyr Asp	Leu Ser Thr Ser Gly Ser Gly		
180	185	190	
Ser Gly Leu Pro Leu Phe Val Gln Arg	Thr Val Ala Arg Thr Ile Val		
195	200	205	
Leu Gln Glu Ile Ile Gly Lys Gly Arg	Phe Gly Glu Val Trp Arg Gly		
210	215	220	
Arg Trp Arg Gly Gly Asp Val Ala Val	Lys Ile Phe Ser Ser Arg Glu		
225	230	235	240
Glu Arg Ser Trp Phe Arg Glu Ala Glu	Ile Tyr Gln Thr Val Met Leu		
245	250	255	
Arg His Glu Asn Ile Leu Gly Phe Ile	Ala Ala Asp Asn Lys Asp Asn		
260	265	270	
Gly Thr Trp Thr Gln Leu Trp Leu Val	Ser Asp Tyr His Glu His Gly		
275	280	285	
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr	Thr Val Thr Ile Glu Gly Met		
290	295	300	
Ile Lys Leu Ala Leu Ser Ala Ala Ser	Gly Leu Ala His Leu His Met		
305	310	315	320
Glu Ile Val Gly Thr Gln Gly Lys Pro	Gly Ile Ala His Arg Asp Leu		
325	330	335	
Lys Ser Lys Asn Ile Leu Val Lys Lys	Asn Gly Met Cys Ala Ile Ala		
340	345	350	
Asp Leu Gly Leu Ala Val Arg His Asp	Ala Val Thr Asp Thr Ile Asp		
355	360	365	
Ile Ala Pro Asn Gln Arg Val Gly	Thr Lys Arg Tyr Met Ala Pro Glu		
370	375	380	
Val Leu Asp Glu Thr Ile Asn Met Lys	His Phe Asp Ser Phe Lys Cys		
385	390	395	400
Ala Asp Ile Tyr Ala Leu Gly Leu Val	Tyr Trp Glu Ile Ala Arg Arg		
405	410	415	
Cys Asn Ser Gly Gly Val His Glu Asp	Tyr Gln Leu Pro Tyr Tyr Asp		
420	425	430	
Leu Val Pro Ser Asp Pro Ser Ile	Glu Met Arg Lys Val Val Cys		
435	440	445	
Asp Gln Lys Leu Arg Pro Asn Val Pro	Asn Trp Trp Gln Ser Tyr Glu		
450	455	460	
Ala Leu Arg Val Met Gly Lys Met Met	Arg Glu Cys Trp Tyr Ala Asn		
465	470	475	480
Gly Ala Ala Arg Leu Thr Ala Leu Arg	Ile Lys Lys Thr Leu Ser Gln		
485	490	495	
Leu Ser Val Gln Glu Asp Val Lys Ile			
500	505		

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1952 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGGCGGC	AGAACGTTGCC	GGCGTGGTGC	TCGTAGTGAG	GGCGCGGAGG	ACCCGGGACC	60
TGGGAAGCGG	CGGCGGGTTA	ACTTCGGCTG	AATCACAAACC	ATTGGCGCT	GAGCTATGAC	120
AAGAGAGCAA	ACAAAAAAGTT	AAAGGAGCAA	CCCGCCATA	AGTGAAGAGA	GAAAGTTATT	180
GATAAC ATG	CTC TTA CGA	AGC TCT GGA	AAA TTA AAT	GTG GGC ACC	AAG	228
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys						
1	5	10				
AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA						276
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu						
15	20	25	30			
CGT TGT AAA TGC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC						324
Arg Cys Lys Cys His His Cys Pro Glu Asp Ser Val Asn Asn Ile						
35	40	45				
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT						372
Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser						
50	55	60				
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT						420
Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Gly Ser Asp						
65	70	75				
TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA						468
Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu						
80	85	90				
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG						516
Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu						
95	100	105	110			
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG						564
Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys						
115	120	125				
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT						612
Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile						
130	135	140				
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG						660
Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg						
145	150	155				
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG						708
Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu						
160	165	170				
TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA						756
Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser						
175	180	185	190			
GGC CTC CCT CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG						804
Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met						
195	200	205				
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG						852
Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys						
210	215	220				
TGG CGT GGA AAG GTG GCT GTG AAA GTG TTC ACC ACG GAG GAA						900
Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu						
225	230	235				
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG						948
Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg						
240	245	250				

CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG	996
His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly	
255 260 265 270	
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC	1044
Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser	
275 280 285	
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG	1092
Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu	
290 295 300	
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA	1140
Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu	
305 310 315	
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA	1188
Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
320 325 330	
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
370 375 380	
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	
385 390 395	
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT	1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys	
400 405 410	
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG	1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu	
415 420 425 430	
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG	1524
Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met	
435 440 445	
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT	1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
450 455 460	
CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT	1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
465 470 475	
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG	1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
480 485 490	
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA	1722
Ser Glu Ser Gln Asp Ile Lys Leu	
495 500	
ATTTCACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCC AGTGAGTTCA	1782
GACTTTCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCTAT	1842
CATGGCTTTC TGAGGAGGGAG AAACCTGTTG GGTAACCTGT TCAAGATATG ATGCATGTTG	1902
CTTTCTAACAGA AAGCCCTGTA TTTTGAATTA CCATTTTTT ATAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu
1 5 10 15
Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys
20 25 30
Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
35 40 45
Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met
50 55 60
Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
65 70 75 80
Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
85 90 95
Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
100 . 105 110
Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu
115 120 125
Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
130 135 140
Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser
145 150 155 160
Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
165 170 175
Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
180 185 190
Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
195 200 205
Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
210 215 220
Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
225 230 235 240
Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
245 250 255
Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
260 265 270
Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
275 280 285
Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
290 295 300
Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
305 310 315 320
Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
325 330 335
Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
340 345 350
Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
355 360 365
Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
370 375 380
Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met
385 390 395 400
Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser
405 410 415
Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro

420	425	430
Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys		
435	440	445
Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg		
450	455	460
Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser		
465	470	475
Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu		480
485	490	495
Ser Gln Asp Ile Lys Leu		
500		

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
CGGAATTCTG GTGCCATATA

20

(2) INFORMATION FOR SEQ ID NO: 23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
ATTCAAGGGC ACATCAACTT CATTGTGTC ACTGTTG

37

(2) INFORMATION FOR SEQ ID NO: 24:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
GCGGATCCAC CATGGCGGAG TCGGCC

26

(2) INFORMATION FOR SEQ ID NO: 25:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
Gly Xaa Gly Xaa Xaa Gly

1

5

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn

1 5

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn

1 5

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met

1 5

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
5 10 15
Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
20 25 30
Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
35 40 45
Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
50 55 60
Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
65 70 75 80
Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
85 90 95
Ser Pro Glu Val Tyr Phe Cys Cys Glu Gly Asn Met Cys Asn Glu
100 105 110
Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn

115	120	125
Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile	Leu Leu Tyr Ser Leu	
130	135	140
Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile	Cys Ala Phe Trp Val	
145	150	155
Tyr Arg His His Lys Met Ala Tyr Pro Pro Val	Leu Val Pro Thr Gln	160
165	170	175
Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly	Leu Lys Pro Leu	
180	185	190
Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe	Gly Cys Val Trp Lys	
195	200	205
Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys	Ile Phe Pro Ile Gln	
210	215	220
Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val	Tyr Ser Leu Pro Gly	
225	230	235
Met Lys His Glu Asn Ile Leu Gln Phe Ile	Gly Ala Glu Lys Arg Gly	240
245	250	255
Thr Ser Val Asp Val Asp Leu Trp Leu Ile	Thr Ala Phe His Glu Lys	
260	265	270
Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val	Val Ser Trp Asn Glu	
275	280	285
Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly	Leu Ala Tyr Leu His	
290	295	300
Glu Asp Ile Pro Gly Leu Lys Asp Gly His	Lys Pro Ala Ile Ser His	
305	310	315
Arg Asp Ile Lys Ser Lys Asn Val Leu Lys	Asn Asn Leu Thr Ala	320
325	330	335
Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys	Phe Glu Ala Gly Lys Ser	
340	345	350
Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg	Arg Tyr Met Ala Pro	
355	360	365
Glu Val Leu Glu Gly Ala Ile Asn Phe Gln	Arg Asp Ala Phe Leu Arg	
370	375	380
Ile Asp Met Tyr Ala Met Gly Leu Val Leu	Trp Glu Leu Ala Ser Arg	
385	390	395
Cys Thr Ala Ala Asp Gly Pro Val Asp Glu	Tyr Met Leu Pro Phe Glu	
405	.	410
415		
Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp	Met Gln Glu Val Val	
420	425	430
Val His Lys Lys Arg Pro Val Leu Arg Asp	Tyr Trp Gln Lys His	
435	440	445
Ala Gly Met Ala Met Leu Cys Glu Thr Ile	Glu Glu Cys Trp Asp His	
450	455	460
Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys	Val Gly Glu Arg Ile Thr	
465	470	475
Gln Met Gln Arg Leu Thr Asn Ile Ile	Thr Thr Glu Asp Ile Val Thr	480
485	490	495
Val Val Thr Met Val Thr Asn Val Asp Phe	Pro Pro Lys Glu Ser Ser	
500	505	510
Leu		

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
5 10 15
Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
20 25 30
Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
35 40 45
Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
50 55 60
Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
65 70 75 80
Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
85 90 95
Pro Gln Val Tyr Phe Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
100 105 110
Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
115 120 125
Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
130 135 140
Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
145 150 155 160
Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
165 170 175
Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe
180 185 190
Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu
195 200 205
Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
210 215 220
Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val
225 230 235 240
Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu
245 250 255
Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile
260 265 270
Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile
275 280 285
Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn
290 295 300
Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
305 310 315 320
Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
325 330 335
His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
340 345 350
Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
355 360 365
Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
370 375 380
Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
385 390 395 400
Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
405 410 415
Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp
420 425 430
Glu Tyr Met Leu Pro Phe Glu Glu Ile Gly Gln His Pro Ser Leu

435	440	445
Glu Glu Leu Gln Glu Val Val Val His Lys Lys Met Arg Pro Thr Ile		
450	455	460
Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr		
465	470	475
Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly		
485	490	495
Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr		
500	505	510
Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp		
515	520	525
Leu Leu Pro Lys Glu Ser Ser Ile		
530	535	

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu		
5	10	15
Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val		
20	25	30
Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro		
35	40	45
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln		
50	55	60
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro		
65	70	75
Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr		
85	90	95
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile		
100	105	110
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys		
115	120	125
Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn		
130	135	140
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu		
145	150	155
Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu		
165	170	175
Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn		
180	185	190
Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys		
195	200	205
Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg		
210	215	220
Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu		
225	230	235
Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala		
245	250	255
Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu		
260	265	270
Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys		

275	280	285
Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His	Glu Asn Ile	
290	295	300
Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln		
305	310	315
Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr		320
325	330	335
Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser		
340	345	350
Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys		
355	360	365
Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn		
370	375	380
Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu		
385	390	395
Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser		
405	410	415
Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser		
420	425	430
Arg Met Asn Leu Glu Asn Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr		
435	440	445
Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val		
450	455	460
Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu		
465	470	475
His Pro Cys Val Glu Ser Met Lys Asp Asn Val Leu Arg Asp Arg Gly		
485	490	495
Arg Pro Glu Ile Pro Ser Phe Trp Leu Asn His Gln Gly Ile Gln Met		
500	505	510
Val Cys Glu Thr Leu Thr Glu Cys Trp Asp His Asp Pro Glu Ala Arg		
515	520	525
Leu Thr Ala Gln Cys Val Ala Glu Arg Phe Ser Glu Leu Glu His Leu		
530	535	540
Asp Arg Leu Ser Gly Arg Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp		
545	550	555
Gly Ser Leu Asn Thr Thr Lys		
565		

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly Asn Val Ser Arg Gly		
5	10	15
Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Ile Asp		
20	25	30
Glu Pro Ala Phe His Lys Glu Ile Glu Ile Phe Glu Thr Arg Met Leu		
35	40	45
Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr		
50	55	60
Gly Phe Val Thr Glu Leu Trp Leu Val Ile Glu Tyr His Pro Ser Gly		
65	70	75
Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr		80

85	90	95
Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu Ala Phe Leu His Asn		
100	105	110
Gln Ile Gly Gly Ser Lys Glu Ser Asn Lys Pro Ala Met Ala His Arg		
115	120	125
Asp Ile Lys Ser Lys Asn Ile Met Tyr Lys Asn Asp Leu Thr Cys Ala		
130	135	140
Ile Gly Asp Leu Gly Leu Ser Leu Ser Lys Pro Glu Asp Ala Ala Ser		
145	150	155
Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly Thr Val Arg Tyr Leu		
165	170	175
Ala Pro		

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

Thr Arg Leu His Leu Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala		
5	10	15
Arg Thr Thr Gly Trp Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp		
20	25	30
Arg Ser Phe Tyr Glu Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln		
35	40	45
Ser Ala Arg Pro Ser Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu		
50	55	60
Lys Ser Val Thr Asp Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val		
65	70	75
Cys Thr Asn Asn Thr Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys		
85	90	95
Asp Lys Gly Asn Phe Cys Ala Asn Glu Thr Ile Ile His Leu Ala Pro		
100	105	110
Gly Pro Gln Gln Ser Ser Thr Trp Leu Ile Leu Thr Ile Leu Ala Leu		
115	120	125
Leu Thr		
130		

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Asp Leu Lys Pro Glu Asn
5

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
Asp Leu Ala Ala Arg Asn
5

(2) INFORMATION FOR SEQ ID NO: 37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
Gly Thr Xaa Xaa Tyr Xaa
5

(2) INFORMATION FOR SEQ ID NO: 38:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
Gly Thr Xaa Xaa Phe Xaa
5

(2) INFORMATION FOR SEQ ID NO: 39:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
Gly Ser Xaa Xaa Tyr Xaa
5

(2) INFORMATION FOR SEQ ID NO: 40:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
Gly Ser Xaa Xaa Phe Xaa
5

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Xaa Pro Ile Lys Trp Thr

5

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Xaa Pro Ile Lys Trp Met

5

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Xaa Pro Ile Arg Trp Thr

5

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Xaa Pro Ile Arg Trp Met

5

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Xaa Pro Val Lys Trp Thr

5

(2) INFORMATION FOR SEQ ID NO: 46:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Xaa Pro Val Lys Trp Met

5

(2) INFORMATION FOR SEQ ID NO: 47:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Xaa Pro Val Arg Trp Thr

5

(2) INFORMATION FOR SEQ ID NO: 48:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Xaa Pro Val Arg Trp Met

5